

SEQUENCE LISTING

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DIJKHUIZEN, LUBBERT  
RAHAOUI, HAKIM

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<170> PatentIn Ver. 2.1

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Val Gly Tyr Val Ala Asp Ser Leu Thr Gly Ser Tyr Lys Pro Leu Asn			
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tttggccatc tttgtcgg 2592

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1 5

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20 25

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<212> PRT  
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1 5 10 15

<210> 8  
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<212> PRT  
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<400> 8

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1 5

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<212> PRT  
<213> Lactobacillus reuteri

<400> 9  
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1 5 10 15

Glu Val Glu

<210> 10  
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aatgtgccta ggatgcataa tggatgtaaa ttactagatg gcggtttta tacattaacc 180  
tcgcaggaga gaaaagaagc aattagtaag gatccatatg cagataaatt tattaggcct 240  
tatttaggtg ctaaaaattt cattcatgga actgcttagt actgtatttg gttaaaggac 300  
gcaaaccgc aagatatcca tcaatcgcca tttatactgg atagaatcaa taaagtagcg 360  
gaattcagat cgcagaaaa aagtaaagat acacaaaaat atgcaaaacg gcccattgcta 420  
acaacacgac ttgccttata tagccacgat gtacatacgg atatgctgat agtacctgca 480  
acatcatcgc aacgttagaga atatcttcca attggatatg tttcagaaaa gaatattgtg 540  
tcttattcac taatgcta atcccaatgct agtaattta atttcggtat tctagaatct 600  
aaagttcact atatttggtt aaaaaacttt tgcggcggt tgaagtccga ttatcggtat 660

tcaaacacta ttatccataa taatccct tggccgactg ttggtgacaa gccaggamca 720  
 acaccatctc tgacactcgc tcaaggata ttaaatactc gcaagctcta tccagacagc 780  
 tcactggctg atcttatga tccactaaca atgccragtt gaactcgtaa agctcatgaa 840  
 gccaatgata aagctgttct taaagcatat ggattgagcc ctaaagctac tgagcaagaa 900  
 atcgtagaac atctattaa gatgtatgaa aaactgacta aaggtgaaag ataactttgt 960  
 aaaaccaata ttttataaag acagtaaatg ttaatttgat aaaaacatat attaataaaa 1020  
 caaaaagtat ataatcaagt agttttgtt attacaaaat acatthaata tcttcagca 1080  
 tttgcatac tgggagattt tttattgaca aattgtttga aagtgttat gatgaaaccg 1140  
 ttagaaact aattcaattt gataaacgtt agacatttct gaggaggaag tcatttgaa 1200  
 gtacaaagaa cataagaaa atg tat aaa gtc ggc aag aat tgg gcc gtt gct 1252  
                   Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala  
                   1                  5                  10

aca ttg gta tca gct tca att tta atg gga ggg gtt gta acc gct cat 1300  
 Thr Leu Val Ser Ala Ser Ile Leu Met Gly Gly Val Val Thr Ala His  
                   15                  20                  25

gct gat caa gta gaa agt aac aat tac aac ggt gtt gct gaa gtt aat 1348  
 Ala Asp Gln Val Glu Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn  
                   30                  35                  40

act gaa cgt caa gct aat ggt caa att ggc gta gat gga aaa att att 1396  
 Thr Glu Arg Gln Ala Asn Gln Ile Gly Val Asp Gly Lys Ile Ile  
                   45                  50                  55

agt gct aac agt aat aca acc agt ggc tcg aca aat caa gaa tca tct 1444  
 Ser Ala Asn Ser Asn Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser  
                   60                  65                  70                  75

gct act aac aat act gaa aat gct gtt gtt aat gaa agc aaa aat act 1492  
 Ala Thr Asn Asn Thr Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr  
                   80                  85                  90

aac aat act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aat 1540  
 Asn Asn Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn  
                   95                  100                  105

act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aac aca gaa 1588  
 Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu  
                   110                  115                  120

aac gat aat agt caa tta aag tta act aat aat gaa caa cca tca gcc 1636  
 Asn Asp Asn Ser Gln Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala  
                   125                  130                  135

gct act caa gca aac ttg aag aag cta aat cct caa gct gct aag gct 1684  
 Ala Thr Gln Ala Asn Leu Lys Leu Asn Pro Gln Ala Ala Lys Ala  
                   140                  145                  150                  155

gtt caa aat gcc aag att gat gcc ggt agt tta aca gat gat caa att 1732  
 Val Gln Asn Ala Lys Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile

160	165	170	
aat gaa tta aat aag att aac ttc tct aag tct gct gaa aag ggt gca Asn Glu Leu Asn Lys Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala			1780
175	180	185	
aaa ttg acc ttt aag gac tta gag ggg att ggt aat gct att gtt aag Lys Leu Thr Phe Lys Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys			1828
190	195	200	
caa gat cca caa tat gct att cct tat tct aat gct aag gaa atc aag Gln Asp Pro Gln Tyr Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys			1876
205	210	215	
aat atg cct gca aca tac act gta gat gcc caa aca ggt aag atg gct Asn Met Pro Ala Thr Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala			1924
220	225	230	235
cat ctt gat gtc tgg gac tct tgg cca gta caa gat cct gtc aca ggt His Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly			1972
240	245	250	
tat gta tct aat tac atg ggt tat caa cta gtt att gct atg atg ggt Tyr Val Ser Asn Tyr Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly			2020
255	260	265	
att cca aat tcg cca act gga gat aat cat atc tat ctt ctt tac aac Ile Pro Asn Ser Pro Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn			2068
270	275	280	
aag tat ggt gat aat gac ttt tct cat tgg cgc aat gca ggt tca atc Lys Tyr Gly Asp Asn Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile			2116
285	290	295	
ttt gga act aaa gaa aca aat gtg ttc caa gaa tgg tca ggt tca gct Phe Gly Thr Lys Glu Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala			2164
300	305	310	315
att gta aat gat gat ggt aca att caa cta ttt ttc acc tca aat gat Ile Val Asn Asp Asp Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp			2212
320	325	330	
acg tct gat tac aag ttg aat gat caa cgc ctt gct acc gca aca tta Thr Ser Asp Tyr Lys Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu			2260
335	340	345	
aac ctt aat gtt gat gat aac ggt gtt tca atc aag agt gtt gat aat Asn Leu Asn Val Asp Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn			2308
350	355	360	
tat caa gtt ttg ttt gaa ggt gat gga ttt cac tac caa act tat gaa Tyr Gln Val Leu Phe Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu			2356
365	370	375	
caa ttc gca aac ggc aaa gat cgt gaa aat gat gat tac tgc tta cgt Gln Phe Ala Asn Gly Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg			2404
380	385	390	395
gac cca cac gtt caa tta gaa aat ggt gat cgt tat ctt gta ttc Asp Pro His Val Val Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe			2452
400	405	410	

gaa gct aat act ggg aca gaa gat tac caa agt gac gac caa att tat Glu Ala Asn Thr Gly Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr 415 420 425	2500
aat tgg gct aac tat ggt ggc gat gat gcc ttc aat att aag agt tcc Asn Trp Ala Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser 430 435 440	2548
ttc aag ctt ttg aat aat aag aag gat cgt gaa ttg gct ggt tta gct Phe Lys Leu Leu Asn Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala 445 450 455	2596
aat ggt gca ctt ggt atc tta aag ctc act aac aat caa agt aag cca Asn Gly Ala Leu Gly Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro 460 465 470 475	2644
aag gtt gaa gaa gta tac tca cca ttg gta tct act ttg atg gct tgc Lys Val Glu Glu Val Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys 480 485 490	2692
gat gag gta nnn nnn aag ctt ggt gat aag tat tat ctc ttc tcc gta Asp Glu Val Xaa Xaa Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val 495 500 505	2740
act cgt gta agt cgt ggt tcc gat cgt gaa tta acc gct aag gat aac Thr Arg Val Ser Arg Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn 510 515 520	2788
aca atc gtt ggt gat aac gtt gct atg att ggt tac gtt tcc gat agc Thr Ile Val Gly Asp Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser 525 530 535	2836
tta atg ggt aag tac aag cca tta aat aac tca ggt gtc gta tta act Leu Met Gly Lys Tyr Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr 540 545 550 555	2884
gca tca gta cct gca aac tgg cgt act gct act tat tcc tac tat gca Ala Ser Val Pro Ala Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Tyr Ala 560 565 570	2932
gta cct gta gct ggt cat cct gat caa gta tta att act tct tac atg Val Pro Val Ala Gly His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met 575 580 585	2980
agt aac aag gac ttt gct tca ggt gaa gga aac tat gca act tgg gca Ser Asn Lys Asp Phe Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala 590 595 600	3028
cca agt ttc tta gta caa atc aat cca gat gac acg aca act gta tta Pro Ser Phe Leu Val Gln Ile Asn Pro Asp Asp Thr Thr Val Leu 605 610 615	3076
gca cgt gca act aac caa ggt gac tgg gtg tgg gac gac tct agt cgg Ala Arg Ala Thr Asn Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg 620 625 630 635	3124
aac gat aat atg ctc ggt gtt ctt aaa gaa ggt gca gct aac agt gcc Asn Asp Asn Met Leu Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala 640 645 650	3172

gcc tta cca ggt gaa tgg ggt aag cca gtt gac tgg agt ttg att aac 3220  
 Ala Leu Pro Gly Glu Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn  
 655 660 665

aga agt cct ggc tta ggc tta aag cct cat caa cca gtt caa cca aag 3268  
 Arg Ser Pro Gly Leu Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys  
 670 675 680

att gat caa cct gat caa caa cct tct ggt caa aac act aag aat gtc 3316  
 Ile Asp Gln Pro Asp Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val  
 685 690 695

aca cca ggt aat ggt gat aag cct gct ggt aag gca act cct gat aac 3364  
 Thr Pro Gly Asn Gly Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn  
 700 705 710 715

act aat att gat cca agt gca caa cct tct ggt caa aac act aat att 3412  
 Thr Asn Ile Asp Pro Ser Ala Gln Pro Ser Gly Gln Asn Thr Asn Ile  
 720 725 730

gat cca agt gca caa mct tct ggt caa aac act aag aat gtc aca cca 3460  
 Asp Pro Ser Ala Gln Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro  
 735 740 745

ggt aat gag aaa caa ggt aag aat acc gat gca aaa caa tta cca caa 3508  
 Gly Asn Glu Lys Gln Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln  
 750 755 760

aca ggt aat aag tct ggt tta gca gga ctt tac gct ggt tca tta ctt 3556  
 Thr Gly Asn Lys Ser Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu  
 765 770 775

gcc ttg ttt gga ttg gca gca att gaa aag cgt cac gct taa 3598  
 Ala Leu Phe Gly Leu Ala Ala Ile Glu Lys Arg His Ala  
 780 785 790

tagagtaaaa aaacatccctc cactcaagtt acaagtagga taatatgtat tatttctacg 3658

cytagtcaag agratttact ggacatannn nnnnnnnnnn tccagttacc aagtggata 3718

tagtattatt ccacgctagt caggaggatt actgacattt ttggctacat ggccggtagt 3778

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atatgggtt tcataattta acactttcg aggacggcgg ttcagctgat gttggcagaa 3898

actgacgtcc ttatctgtat aatcatcaat attagccctt ttaggaaagt attccctaat 3958

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tggagtcaat gaatggacaa attctttagg aatagaccct aagagatcaa ttaagccctg 4138

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<223> Any amino acid

<220>  
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Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala  
35 40 45  
  
Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile Ser Ala Asn Ser Asn  
50 55 60  
  
Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser Ala Thr Asn Asn Thr  
65 70 75 80  
  
Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr Asn Asn Thr Glu Asn  
85 90 95  
  
Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Ala Val  
100 105 110  
  
Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Asp Asn Ser Gln  
115 120 125  
  
Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala Ala Thr Gln Ala Asn  
130 135 140  
  
Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala Val Gln Asn Ala Lys  
145 150 155 160  
  
Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile Asn Glu Leu Asn Lys  
165 170 175

Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala Lys Leu Thr Phe Lys  
180 185 190

Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys Gln Asp Pro Gln Tyr  
195 200 205

Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys Asn Met Pro Ala Thr  
210 215 220

Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala His Leu Asp Val Trp  
225 230 235 240

Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly Tyr Val Ser Asn Tyr  
245 250 255

Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly Ile Pro Asn Ser Pro  
260 265 270

Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn Lys Tyr Gly Asp Asn  
275 280 285

Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile Phe Gly Thr Lys Glu  
290 295 300

Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala Ile Val Asn Asp Asp  
305 310 315 320

Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp Thr Ser Asp Tyr Lys  
325 330 335

Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu Asn Leu Asn Val Asp  
340 345 350

Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn Tyr Gln Val Leu Phe  
355 360 365

Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu Gln Phe Ala Asn Gly  
370 375 380

Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg Asp Pro His Val Val  
385 390 395 400

Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe Glu Ala Asn Thr Gly  
405 410 415

Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr Asn Trp Ala Asn Tyr  
420 425 430

Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser Phe Lys Leu Leu Asn  
435 440 445

Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala Asn Gly Ala Leu Gly  
450 455 460

Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro Lys Val Glu Glu Val  
465 470 475 480

Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys Asp Glu Val Xaa Xaa  
485 490 495

Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val Thr Arg Val Ser Arg

500

505

510

Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn Thr Ile Val Gly Asp  
515 520 525

Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser Leu Met Gly Lys Tyr  
530 535 540

Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr Ala Ser Val Pro Ala  
545 550 555 560

Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Tyr Ala Val Pro Val Ala Gly  
565 570 575

His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met Ser Asn Lys Asp Phe  
580 585 590

Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala Pro Ser Phe Leu Val  
595 600 605

Gln Ile Asn Pro Asp Asp Thr Thr Val Leu Ala Arg Ala Thr Asn  
610 615 620

Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg Asn Asp Asn Met Leu  
625 630 635 640

Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala Ala Leu Pro Gly Glu  
645 650 655

Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn Arg Ser Pro Gly Leu  
660 665 670

Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys Ile Asp Gln Pro Asp  
675 680 685

Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val Thr Pro Gly Asn Gly  
690 695 700

Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn Thr Asn Ile Asp Pro  
705 710 715 720

Ser Ala Gln Pro Ser Gly Gln Asn Thr Asn Ile Asp Pro Ser Ala Gln  
725 730 735

Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro Gly Asn Glu Lys Gln  
740 745 750

Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln Thr Gly Asn Lys Ser  
755 760 765

Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu Ala Leu Phe Gly Leu  
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785 790

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
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<210> 14  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
gtgatacatt tccatttatta tcag 24

<210> 15  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
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<210> 16  
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<212> DNA  
<213> Artificial Sequence

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<400> 16  
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<210> 17  
<211> 38  
<212> DNA  
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<220>  
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38

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<222> (6)  
<223> a, c, t, g, other or unknown

<220>  
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<222> (15)  
<223> a, c, t, g, other or unknown

<400> 18  
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21

<210> 19  
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<212> DNA  
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<220>  
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<220>  
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<223> a, c, t, g, other or unknown

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23

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<220>
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<210> 21
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 21
cctgtccgaa catcttgaac tg 22

<210> 22
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<212> DNA
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<220>
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<220>
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<220>
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<220>
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<223> a, c, t, g, other or unknown

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<220>
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<223> a, c, t, g, other or unknown

<220>
<221> modified_base
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<223> a, c, t, g, other or unknown

<400> 23
tayaayggng tngcngargt naa
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23

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<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ccgaccatct tgtttgattt ac
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22

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<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
aaytataayg gygttgccryg aagt
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24

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<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>  
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<220>  
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<400> 26  
tacccgnwsnc tacttcaact t 21

<210> 27  
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<213> Lactobacillus reuteri

<400> 27  
Tyr Asn Gly Val Ala Glu Val Lys Lys Arg Gly Tyr Phe Tyr Ala Arg  
1 5 10 15

Thr

<210> 28  
<211> 17  
<212> PRT  
<213> Lactobacillus reuteri

<400> 28  
Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala Asn Gly Gly  
1 5 10 15

Ile

<210> 29  
<211> 14  
<212> PRT  
<213> Bacillus amyloliquefaciens

<400> 29  
Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp  
1 5 10

<210> 30  
<211> 14  
<212> PRT  
<213> Bacillus subtilis

<400> 30  
Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp  
1 5 10

<210> 31  
<211> 14  
<212> PRT  
<213> Streptococcus mutans

<400> 31  
Asp Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Ala Lys  
1 5 10

<210> 32  
<211> 14  
<212> PRT  
<213> *Streptococcus salivarius*

<400> 32  
Glu Ile Asp Val Trp Asp Ser Trp Pro Val Gln Asp Ala Lys  
1 5 10

<210> 33  
<211> 16  
<212> PRT  
<213> *Bacillus amyloliquefaciens*

<400> 33  
Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp Gly Lys  
1 5 10 15

<210> 34  
<211> 16  
<212> PRT  
<213> *Bacillus subtilis*

<400> 34  
Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp Gly Lys  
1 5 10 15

<210> 35  
<211> 16  
<212> PRT  
<213> *Streptococcus mutans*

<400> 35  
Leu Thr Gln Glu Trp Ser Gly Ser Ala Thr Val Asn Glu Asp Gly Ser  
1 5 10 15

<210> 36  
<211> 16  
<212> PRT  
<213> *Streptococcus salivarius*

<400> 36  
Asp Asp Gln Gln Trp Ser Gly Ser Ala Thr Val Asn Ser Asp Gly Ser  
1 5 10 15

<210> 37  
<211> 11  
<212> PRT  
<213> *Bacillus amyloliquefaciens*

<400> 37

Lys Ala Thr Phe Gly Pro Ser Phe Leu Met Asn  
1 5 10

<210> 38  
<211> 11  
<212> PRT  
<213> *Bacillus subtilis*

<400> 38  
Gln Ser Thr Phe Ala Pro Ser Phe Leu Leu Asn  
1 5 10

<210> 39  
<211> 11  
<212> PRT  
<213> *Streptococcus mutans*

<400> 39  
Asn Ser Thr Trp Ala Pro Ser Phe Leu Ile Gln  
1 5 10

<210> 40  
<211> 11  
<212> PRT  
<213> *Streptococcus salivarius*

<400> 40  
Lys Ser Thr Trp Ala Pro Ser Phe Leu Ile Lys  
1 5 10